



SEQUENCE LISTING

<110> ZOLLER, MARK
LI, XIAODONG
STASZEWSKI, LENA
O'CONNELL, SHAWN
ZOZULYA, SERGEY
ADLER, JON
XU, HONG
ECHEVERRI, FERNANDO

<120> T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
IDENTIFICATION OF TASTE COMPOUNDS

<130> 67824.407404

<140> 10/725,473
<141> 2003-12-03

<150> 10/179,373
<151> 2002-06-26

<150> 60/300,434
<151> 2001-06-26

<150> 09/897,427
<151> 2001-07-03

<150> 60/304,749
<151> 2001-07-13

<150> 60/310,493
<151> 2001-08-08

<150> 60/331,771
<151> 2001-11-21

<150> 60/339,472
<151> 2001-12-14

<150> 10/035,045
<151> 2002-01-03

<150> 60/372,090
<151> 2002-04-15

<150> 60/374,143
<151> 2002-04-22

<160> 19

<170> PatentIn Ver. 3.3

<210> 1
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic PDZIP
 sequence

<400> 1
 Ser Val Ser Thr Trp
 1 5

<210> 2
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic consensus
 sequence

<220>
 <221> MOD_RES
 <222> (1)
 <223> Thr or Arg

<220>
 <221> MOD_RES
 <222> (3)
 <223> Phe or Leu

<220>
 <221> MOD_RES
 <222> (4)
 <223> Arg, Gln or Pro

<220>
 <221> MOD_RES
 <222> (6)
 <223> Arg or Thr

<220>
 <221> MOD_RES
 <222> (7)
 <223> Ser, Pro or Val

<220>
 <221> MOD_RES
 <222> (8)
 <223> Val, Glu, Arg, Lys or Thr

```
<220>
<221> MOD_RES
<222> (11)
<223> Ala or Glu
```

```
<220>
<221> MOD_RES
<222> (12)
<223> Trp or Leu
```

```
<220>
<221> MOD_RES
<222> (13)
<223> Arg, His or Gly
```

<400> 2
Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu
1 5 10

```
<210> 3
<211> 15
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic consensus sequence

```
<220>
<221> MOD_RES
<222> (1)
<223> Leu or Gln
```

```
<220>
<221> MOD_RES
<222> (3)
<223> Glu, Gly or Thr
```

```
<220>
<221> MOD_RES
<222> (4)
<223> Asn, Arg or Cys
```

```
<220>
<221> MOD_RES
<222> (7)
<223> Arg or Glu
```

```
<220>
<221> MOD_RES
<222> (9)
<223> Arg or Lys
```

<220>
 <221> MOD_RES
 <222> (10)
 <223> Cys, Gly or Phe

<220>
 <221> MOD_RES
 <222> (11)
 <223> Val, Leu or Ile

<220>
 <221> MOD_RES
 <222> (13)
 <223> Phe or Leu

<220>
 <221> MOD_RES
 <222> (14)
 <223> Ala or Ser

<220>
 <221> MOD_RES
 <222> (15)
 <223> Met or Leu

<400> 3
 Xaa Pro Xaa Xaa Tyr Asn Xaa Ala Xaa Xaa Xaa Thr Xaa Xaa Xaa
 1 5 10 15

<210> 4
 <211> 858
 <212> PRT
 <213> Rattus sp.

<400> 4
 Met Pro Gly Leu Ala Ile Leu Gly Leu Ser Leu Ala Ala Phe Leu Glu
 1 5 10 15

Leu Gly Met Gly Ser Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
 20 25 30

Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Thr Thr Glu Glu
 35 40 45

Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Gly Ile Leu Cys Thr Arg
 50 55 60

Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
 65 70 75 80

Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
 85 90 95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Pro
 100 105 110
 Ser Leu Met Phe Met Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
 115 120 125
 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
 130 135 140
 His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
 145 150 155 160
 Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
 165 170 175
 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
 180 185 190
 Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
 195 200 205
 Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser
 210 215 220
 Ile Phe Ser Gly Leu Ala Asn Ser Arg Gly Ile Cys Ile Ala His Glu
 225 230 235 240
 Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
 245 250 255
 Val Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val
 260 265 270
 Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
 275 280 285
 Leu His Asp Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
 290 295 300
 Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
 305 310 315 320
 Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
 325 330 335
 Tyr Val Glu Thr Arg Leu Ala Leu Ala Ala Asp Pro Thr Phe Cys Ala
 340 345 350
 Ser Leu Lys Ala Glu Leu Asp Leu Glu Glu Arg Val Met Gly Pro Arg
 355 360 365
 Cys Ser Gln Cys Asp Tyr Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
 370 375 380

Met Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr
 385 390 395 400
 Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
 405 410 415
 Cys Asn Val Ser His Cys His Thr Ser Glu Pro Val Gln Pro Trp Gln
 420 425 430
 Leu Leu Glu Asn Met Tyr Asn Met Ser Phe Arg Ala Arg Asp Leu Thr
 435 440 445
 Leu Gln Phe Asp Ala Lys Gly Ser Val Asp Met Glu Tyr Asp Leu Lys
 450 455 460
 Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
 465 470 475 480
 Phe Asn Gly Thr Leu Gln Leu Gln His Ser Lys Met Tyr Trp Pro Gly
 485 490 495
 Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
 500 505 510
 Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp
 515 520 525
 Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
 530 535 540
 Pro Cys Gly Lys Asp Gln Trp Ser Pro Glu Lys Ser Thr Thr Cys Leu
 545 550 555 560
 Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Ser
 565 570 575
 Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Thr Leu Ala Ala Leu
 580 585 590
 Gly Leu Phe Val His Tyr Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
 595 600 605
 Gly Ser Leu Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
 610 615 620
 Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser Cys Leu Ala
 625 630 635 640
 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
 645 650 655
 Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser
 660 665 670

Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp Ala Trp Leu
675 680 685

Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys Ala Trp Tyr
690 695 700

Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln Val Leu Pro
705 710 715 720

Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val Ser Leu Gly
725 730 735

Leu Val His Ile Thr Asn Ala Val Leu Ala Phe Leu Cys Phe Leu Gly
740 745 750

Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
755 760 765

Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Ile Trp Val Ser Phe Val
770 775 780

Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
785 790 795 800

Gly Ala Ile Leu Phe Cys Ala Leu Gly Ile Leu Ala Thr Phe His Leu
805 810 815

Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Glu Leu Asn Thr Gln Glu
820 825 830

Phe Phe Leu Gly Arg Ser Pro Lys Glu Ala Ser Asp Gly Asn Ser Gly
835 840 845

Ser Ser Glu Ala Thr Arg Gly His Ser Glu
850 855

<210> 5

<211> 841

<212> PRT

<213> Homo sapiens

<400> 5

Met Leu Leu Cys Thr Ala Arg Leu Val Gly Leu Gln Leu Leu Ile Ser
1 5 10 15

Cys Cys Trp Ala Phe Ala Cys His Ser Thr Glu Ser Ser Pro Asp Phe
20 25 30

Thr Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
35 40 45

Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
50 55 60

Ser	Cys	Ser	Phe	Asn	Glu	His	Gly	Tyr	His	Leu	Phe	Gln	Ala	Met	Arg	
65					70					75					80	
Leu	Gly	Val	Glu	Glu	Ile	Asn	Asn	Ser	Thr	Ala	Leu	Leu	Pro	Asn	Ile	
			85						90					95		
Thr	Leu	Gly	Tyr	Gln	Leu	Tyr	Asp	Val	Cys	Ser	Asp	Ser	Ala	Asn	Val	
		100						105					110			
Tyr	Ala	Thr	Leu	Arg	Val	Leu	Ser	Leu	Pro	Gly	Gln	His	His	Ile	Glu	
		115						120				125				
Leu	Gln	Gly	Asp	Leu	Leu	His	Tyr	Ser	Pro	Thr	Val	Leu	Ala	Val	Ile	
	130					135					140					
Gly	Pro	Asp	Ser	Thr	Asn	Arg	Ala	Ala	Thr	Thr	Ala	Ala	Leu	Leu	Ser	
145					150					155					160	
Pro	Phe	Leu	Val	Pro	Met	Ile	Ser	Tyr	Ala	Ala	Ser	Ser	Glu	Thr	Leu	
			165						170					175		
Ser	Val	Lys	Arg	Gln	Tyr	Pro	Ser	Phe	Leu	Arg	Thr	Ile	Pro	Asn	Asp	
		180						185					190			
Lys	Tyr	Gln	Val	Glu	Thr	Met	Val	Leu	Leu	Leu	Gln	Lys	Phe	Gly	Trp	
	195						200					205				
Thr	Trp	Ile	Ser	Leu	Val	Gly	Ser	Ser	Asp	Asp	Tyr	Gly	Gln	Leu	Gly	
	210					215					220					
Val	Gln	Ala	Leu	Glu	Asn	Gln	Ala	Thr	Gly	Gln	Gly	Ile	Cys	Ile	Ala	
225					230					235					240	
Phe	Lys	Asp	Ile	Met	Pro	Phe	Ser	Ala	Gln	Val	Gly	Asp	Glu	Arg	Met	
			245						250					255		
Gln	Cys	Leu	Met	Arg	His	Leu	Ala	Gln	Ala	Gly	Ala	Thr	Val	Val	Val	
		260						265					270			
Val	Phe	Ser	Ser	Arg	Gln	Leu	Ala	Arg	Val	Phe	Phe	Glu	Ser	Val	Val	
	275						280					285				
Leu	Thr	Asn	Leu	Thr	Gly	Lys	Val	Trp	Val	Ala	Ser	Glu	Ala	Trp	Ala	
	290					295					300					
Leu	Ser	Arg	His	Ile	Thr	Gly	Val	Pro	Gly	Ile	Gln	Arg	Ile	Gly	Met	
305				310						315					320	
Val	Leu	Gly	Val	Ala	Ile	Gln	Lys	Arg	Ala	Val	Pro	Gly	Leu	Lys	Ala	
			325						330					335		
Phe	Glu	Glu	Ala	Tyr	Ala	Arg	Ala	Asp	Lys	Lys	Ala	Pro	Arg	Pro	Cys	
		340						345					350			

His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln
 355 360 365
 Ala Phe Met Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser
 370 375 380
 Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu
 385 390 395 400
 His Gln Leu Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val
 405 410 415
 Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu
 420 425 430
 His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser
 435 440 445
 Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr
 450 455 460
 Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu
 465 470 475 480
 Thr Lys Ile Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val
 485 490 495
 Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe
 500 505 510
 His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu
 515 520 525
 Asn Lys Ser Asp Leu Tyr Arg Cys Gln Pro Cys Gly Lys Glu Glu Trp
 530 535 540
 Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu
 545 550 555 560
 Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu
 565 570 575
 Leu Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu
 580 585 590
 Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met
 595 600 605
 Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly
 610 615 620
 Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu
 625 630 635 640

Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu
645 650 655

Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala
660 665 670

Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala
675 680 685

Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu
690 695 700

Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys
705 710 715 720

Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly
725 730 735

Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu
740 745 750

Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe
755 760 765

Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp
770 775 780

Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu
785 790 795 800

Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu
805 810 815

Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln
820 825 830

Asp Tyr Thr Arg Arg Cys Gly Ser Thr
835 840

<210> 6

<211> 839

<212> PRT

<213> Homo sapiens

<400> 6

Met Gly Pro Arg Ala Lys Thr Ile Cys Ser Leu Phe Phe Leu Leu Trp
1 5 10 15

Val Leu Ala Glu Pro Ala Glu Asn Ser Asp Phe Tyr Leu Pro Gly Asp
20 25 30

Thr Phe Leu Gly Ile Thr Ile Gln Ser Val Pro Ile Pro Gly Phe Ser
 325 330 335
 Glu Phe Arg Glu Trp Gly Pro Gln Ala Gly Pro Pro Pro Leu Ser Arg
 340 345 350
 Thr Ser Gln Ser Tyr Thr Cys Asn Gln Glu Cys Asp Asn Cys Leu Asn
 355 360 365
 Ala Thr Leu Ser Phe Asn Thr Ile Leu Arg Leu Ser Gly Glu Arg Val
 370 375 380
 Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala His Ala Leu His
 385 390 395 400
 Ser Leu Leu Gly Cys Asp Lys Ser Thr Cys Thr Lys Arg Val Val Tyr
 405 410 415
 Pro Trp Gln Leu Leu Glu Glu Ile Trp Lys Val Asn Phe Thr Leu Leu
 420 425 430
 Asp His Gln Ile Phe Phe Asp Pro Gln Gly Asp Val Ala Leu His Leu
 435 440 445
 Glu Ile Val Gln Trp Gln Trp Asp Arg Ser Gln Asn Pro Phe Gln Ser
 450 455 460
 Val Ala Ser Tyr Tyr Pro Leu Gln Arg Gln Leu Lys Asn Ile Gln Asp
 465 470 475 480
 Ile Ser Trp His Thr Val Asn Asn Thr Ile Pro Met Ser Met Cys Ser
 485 490 495
 Lys Arg Cys Gln Ser Gly Gln Lys Lys Lys Pro Val Gly Ile His Val
 500 505 510
 Cys Cys Phe Glu Cys Ile Asp Cys Leu Pro Gly Thr Phe Leu Asn His
 515 520 525
 Thr Glu Asp Glu Tyr Glu Cys Gln Ala Cys Pro Asn Asn Glu Trp Ser
 530 535 540
 Tyr Gln Ser Glu Thr Ser Cys Phe Lys Arg Gln Leu Val Phe Leu Glu
 545 550 555 560
 Trp His Glu Ala Pro Thr Ile Ala Val Ala Leu Leu Ala Ala Leu Gly
 565 570 575
 Phe Leu Ser Thr Leu Ala Ile Leu Val Ile Phe Trp Arg His Phe Gln
 580 585 590
 Thr Pro Ile Val Arg Ser Ala Gly Gly Pro Met Cys Phe Leu Met Leu
 595 600 605

Thr Leu Leu Leu Val Ala Tyr Met Val Val Pro Val Tyr Val Gly Pro
 610 615 620
 Pro Lys Val Ser Thr Cys Leu Cys Arg Gln Ala Leu Phe Pro Leu Cys
 625 630 635 640
 Phe Thr Ile Cys Ile Ser Cys Ile Ala Val Arg Ser Phe Gln Ile Val
 645 650 655
 Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp
 660 665 670
 Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu
 675 680 685
 Lys Met Val Ile Val Val Ile Gly Met Leu Ala Thr Gly Leu Ser Pro
 690 695 700
 Thr Thr Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys
 705 710 715 720
 Asn Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu
 725 730 735
 Leu Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu
 740 745 750
 Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe
 755 760 765
 Tyr Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser
 770 775 780
 Gly Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu
 785 790 795 800
 Leu Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu
 805 810 815
 Phe Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln
 820 825 830
 Gly Tyr Thr Met Arg Arg Asp
 835

<210> 7

<211> 852

<212> PRT

<213> Homo sapiens

<400> 7

Met Leu Gly Pro Ala Val Leu Gly Leu Ser Leu Trp Ala Leu Leu His
 1 5 10 15

Pro Gly Thr Gly Ala Pro Leu Cys Leu Ser Gln Gln Leu Arg Met Lys
 20 25 30
 Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
 35 40 45
 Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
 50 55 60
 Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
 65 70 75 80
 Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
 85 90 95
 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
 100 105 110
 Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr
 115 120 125
 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
 130 135 140
 His Ser Ser Glu Leu Ala Met Val Thr Gly Lys Phe Phe Ser Phe Phe
 145 150 155 160
 Leu Met Pro Gln Val Ser Tyr Gly Ala Ser Met Glu Leu Leu Ser Ala
 165 170 175
 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
 180 185 190
 Gln Leu Thr Ala Ala Ala Glu Leu Leu Gln Glu Phe Gly Trp Asn Trp
 195 200 205
 Val Ala Ala Leu Gly Ser Asp Asp Glu Tyr Gly Arg Gln Gly Leu Ser
 210 215 220
 Ile Phe Ser Ala Leu Ala Ala Ala Arg Gly Ile Cys Ile Ala His Glu
 225 230 235 240
 Gly Leu Val Pro Leu Pro Arg Ala Asp Asp Ser Arg Leu Gly Lys Val
 245 250 255
 Gln Asp Val Leu His Gln Val Asn Gln Ser Ser Val Gln Val Val Leu
 260 265 270
 Leu Phe Ala Ser Val His Ala Ala His Ala Leu Phe Asn Tyr Ser Ile
 275 280 285
 Ser Ser Arg Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ala Trp Leu
 290 295 300

Thr Ser Asp Leu Val Met Gly Leu Pro Gly Met Ala Gln Met Gly Thr
 305 310 315 320
 Val Leu Gly Phe Leu Gln Arg Gly Ala Gln Leu His Glu Phe Pro Gln
 325 330 335
 Tyr Val Lys Thr His Leu Ala Leu Ala Thr Asp Pro Ala Phe Cys Ser
 340 345 350
 Ala Leu Gly Glu Arg Glu Gln Gly Leu Glu Glu Asp Val Val Gly Gln
 355 360 365
 Arg Cys Pro Gln Cys Asp Cys Ile Thr Leu Gln Asn Val Ser Ala Gly
 370 375 380
 Leu Asn His His Gln Thr Phe Ser Val Tyr Ala Ala Val Tyr Ser Val
 385 390 395 400
 Ala Gln Ala Leu His Asn Thr Leu Gln Cys Asn Ala Ser Gly Cys Pro
 405 410 415
 Ala Gln Asp Pro Val Lys Pro Trp Gln Leu Leu Glu Asn Met Tyr Asn
 420 425 430
 Leu Thr Phe His Val Gly Gly Leu Pro Leu Arg Phe Asp Ser Ser Gly
 435 440 445
 Asn Val Asp Met Glu Tyr Asp Leu Lys Leu Trp Val Trp Gln Gly Ser
 450 455 460
 Val Pro Arg Leu His Asp Val Gly Arg Phe Asn Gly Ser Leu Arg Thr
 465 470 475 480
 Glu Arg Leu Lys Ile Arg Trp His Thr Ser Asp Asn Gln Lys Pro Val
 485 490 495
 Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly Gln Val Arg Arg Val Lys
 500 505 510
 Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp Cys Glu Ala Gly Ser
 515 520 525
 Tyr Arg Gln Asn Pro Asp Asp Ile Ala Cys Thr Phe Cys Gly Gln Asp
 530 535 540
 Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys Phe Arg Arg Arg Ser Arg
 545 550 555 560
 Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Leu Leu Leu Leu Leu Leu
 565 570 575
 Ser Leu Ala Leu Gly Leu Val Leu Ala Ala Leu Gly Leu Phe Val His
 580 585 590

His Arg Asp Ser Pro Leu Val Gln Ala Ser Gly Gly Pro Leu Ala Cys
 595 600 605
 Phe Gly Leu Val Cys Leu Gly Leu Val Cys Leu Ser Val Leu Leu Phe
 610 615 620
 Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu Ala Gln Gln Pro Leu Ser
 625 630 635 640
 His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu Phe Leu Gln Ala Ala
 645 650 655
 Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser Trp Ala Asp Arg Leu
 660 665 670
 Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp Leu Val Val Leu Leu Ala
 675 680 685
 Met Leu Val Glu Val Ala Leu Cys Thr Trp Tyr Leu Val Ala Phe Pro
 690 695 700
 Pro Glu Val Val Thr Asp Trp His Met Leu Pro Thr Glu Ala Leu Val
 705 710 715 720
 His Cys Arg Thr Arg Ser Trp Val Ser Phe Gly Leu Ala His Ala Thr
 725 730 735
 Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu Gly Thr Phe Leu Val Arg
 740 745 750
 Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly Leu Thr Phe Ala Met
 755 760 765
 Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val Pro Leu Leu Ala Asn
 770 775 780
 Val Gln Val Val Leu Arg Pro Ala Val Gln Met Gly Ala Leu Leu Leu
 785 790 795 800
 Cys Val Leu Gly Ile Leu Ala Ala Phe His Leu Pro Arg Cys Tyr Leu
 805 810 815
 Leu Met Arg Gln Pro Gly Leu Asn Thr Pro Glu Phe Phe Leu Gly Gly
 820 825 830
 Gly Pro Gly Asp Ala Gln Gly Gln Asn Asp Gly Asn Thr Gly Asn Gln
 835 840 845
 Gly Lys His Glu
 850

<210> 8
 <211> 2526
 <212> DNA
 <213> Homo sapiens

<400> 8
 atgctgctct gcacggctcg cctgggtcggc ctgcagcttc tcatttcctg ctgctggggcc 60
 tttgcctgcc atagcacgga gtctttctct gacttcaccc tccccggaga ttacctcctg 120
 gcaggcctgt tccctctcca ttctggctgt ctgcaggtga ggcacagacc cgagggtgacc 180
 ctgtgtgaca ggtctttag cttcaatgag catggctacc acctcttcca ggctatgcgg 240
 cttgggggtg aggagataaa caactccacg gccctgctgc ccaacatcac cctgggggtac 300
 cagctgtatg atgtgtgttc tgactctgac aatgtgtatg ccacgctgag agtgctctcc 360
 ctgccagggc aacaccacat agagctccaa ggagaccttc tccactattc ccctacgggtg 420
 ctggcagtga ttgggcctga cagcaccaac cgtgctgcca ccacagccgc cctgctgagc 480
 cctttcctgg tgcccatgat tagctatgag gccagcagc agacgctcag cgtgaagcgg 540
 cagtatccct ctttctgag caccatcccc aatgacaagt accaggtgga gaccatggtg 600
 ctgctgctgc agaagttcgg gtggacctgg atctctctgg ttggcagcag tgacgactat 660
 gggcagctag ggggtgcaggc actggagaac caggccactg gtcaggggat ctgcattgct 720
 ttcaaggaca tcatgccctt ctctgccagc gtgggcgatg agaggatgca gtgcctcatg 780
 cgccacctgg cccaggccgg ggccaccgtc gtggttgttt tttccagccg gcagttggcc 840
 aggggtgttt tccagtcctg ggtgctgacc aacctgactg gcaagggtgt ggctgcctca 900
 gaagcctggg cctctccag gcacatcact ggggtgcccg ggatccagcg cattgggatg 960
 gtgctggggc tggccatcca gaagagggtc gtccctggcc tgaaggcgtt tgaagaagcc 1020
 tatgcccggg cagacaagaa ggcccctagg ccttgccaca agggctcctg gtgcagcagc 1080
 aatcagctct gcagagaatg ccaagctttc atggcacaca cgatgccccaa gctcaaagcc 1140
 ttctccatga gttctgccta caacgcatac cgggctgtgt atgcggtggc ccattggcctc 1200
 caccagctcc tgggctgtgc ctctggagct tgttccaggg gccgagtcta cccctggcag 1260
 cttttggagc agatccacaa ggtgcatttc cttctacaca aggacactgt ggcgtttaat 1320
 gacaacagag atccccctag tagctataac ataattgcct gggactggaa tggacccaag 1380
 tggaccttca cggctcctcg ttccctccca tgggtctccag ttcagctaaa cataaatgag 1440
 accaaaaatc agtggcacgg aaaggacaac caggtgccta agtctgtgtg ttccagcgac 1500
 tgtcttgaag ggcaccagcg agtgggttac ggtttccatc actgctgctt tgagtgtgtg 1560
 ccctgtgggg ctgggacctt cctcaacaag agtgacctct acagatgcca gccttgtggg 1620
 aaagaagagt gggcacctga gggaagccag acctgcttcc cgcgactgtt ggtgtttttg 1680
 gctttgcgtg agcacacctc ttgggtgctg ctggcagcta acacgctgct gctgctgctg 1740
 ctgcttggga ctgctggcct gtttgctggt cacctagaca cccctgtggt gaggtcagca 1800
 gggggccgcc tgtgctttct tatgctgggc tccctggcag caggtagtgg cagcctctat 1860
 ggcttctttg gggaaacccac aaggcctgag tgcttgctac gccaggccct ctttgccctt 1920
 ggtttcacca tcttctgtc ctgcctgaca gttcgctcat tccaactaat catcatctt 1980
 aagttttcca ccaaggtacc tacattctac cacgcctggg tccaaaacca cgggtgctggc 2040
 ctgtttgtga tgatcagctc agcggcccag ctgcttatct gtctaacttg gctgggtgtg 2100
 tggacccac tgctgctag ggaataccag cgcttcccc atctggtgat gcttgagtgc 2160
 acagagacca actccctggg cttcatactg gccttctct acaatggcct cctctccatc 2220
 agtgcccttg cctgcagcta cctgggtaag gacttgccag agaactacaa cgaggccaaa 2280
 tgtgtcacct tcagcctgct cttcaacttc gtgtcctgga tcgccttctt caccacggcc 2340
 agcgtctacg acggcaagta cctgcctgag gccaacatga tggctgggct gagcagcctg 2400
 agcagcggct tcggtgggta ttttctgcct aagtgtacg tgatcctctg ccgcccagac 2460
 ctcaacagca cagagcactt ccaggcctcc attcaggact acacgaggcg ctgaggctcc 2520
 acctga 2526

<210> 9
 <211> 2559
 <212> DNA
 <213> Homo sapiens

<400> 9
 atgctggggc ctgctgtcct gggcctcagc ctctgggctc tcctgcaccc tgggacgggg 60
 gccccattgt gcctgtcaca gcaacttagg atgaaggggg actacgtgct gggggggctg 120
 tcccccttgg gcgaggccga ggaggctggc ctccgcagcc ggacacggcc cagcagccct 180
 gtgtgcacca ggttctcctc aaacggcctg ctctgggcac tggccatgaa aatggccgtg 240
 gaggagatca acaacaagtc ggatctgctg cccgggctgc gcctgggcta cgacctcttt 300
 gatacgtgct cggagcctgt ggtggccatg aagcccagcc tcatgttctt ggccaaggca 360
 ggcagccgcg acatcgccgc ctactgcaac tacacgcagt accagccccg tgtgctggct 420
 gtcactgggg cccactcgtc agagctcgcc atggtcaccg gcaagttctt cagcttcttc 480
 ctcattgccc aggtcagcta cgggtgctagc atggagctgc tgagcgcccc ggagaccttc 540
 cctcctttct tccgcaccgt gcccagcgac cgtgtgcagc tgacggccgc cgcggagctg 600
 ctgcaggagt tcggctggaa ctgggtggcc gccctgggca gcgacgacga gtacggccgg 660
 cagggcctga gcatcttctc ggccctggcc gcggcacgcg gcatctgcat cgcgcacgag 720
 ggcttggctg cgctgccccg tgccgatgac tcgcggctgg ggaaggtgca ggacgtcctg 780
 caccaggtga accagagcag cgtgcagggtg gtgctgctgt tcgcctcctg gcacgccgcc 840
 cacgccctct tcaactacag catcagcagc aggtctctgc ccaaggtgtg ggtggccagc 900
 gaggcctggc tgacctctga cctgggtcatg gggctgcccc gcattggcca gatgggcacg 960
 gtgcttggct tcctccagag ggggtgcccc ctgcacgagt tccccagta cgtgaagacg 1020
 cacctggccc tggccaccga cccggccttc tgctctgccc tgggcgagag ggagcagggt 1080
 ctggaggagg acgtggtggg ccagcgctgc ccgcagtgct actgcatcac gctgcagaac 1140
 gtgagcgag ggctaaatca ccaccagacg ttctctgtct acgcagctgt gtatagctg 1200
 gcccaggccc tgcacaacac tcttcagtgc aacgcctcag gctgccccgc gcaggacccc 1260
 gtgaagccct ggcagctcct ggagaacatg tacaacctga ccttccacgt gggcgggctg 1320
 ccgctgcggt tcgacagcag cggaaacgtg gacatggagt acgacctgaa gctgtgggtg 1380
 tggcagggct cagtgccag gctccacgac gtgggcagg tcaacggcag cctcaggaca 1440
 gagcgccctga agatccgctg gcacacgtct gacaaccaga agcccgtgtc ccggtgctcg 1500
 cggcagtgcc aggagggcca ggtgcgcgg gtcaaggggt tccactcctg ctgctacgac 1560
 tgtgtggact gcgagggcgg cagctaccgg caaaacccag acgacatcgc ctgcaccttt 1620
 tgtggccagg atgagtggc cccggagcga agcacacgct gcttccgcgg cagggtctcg 1680
 ttcttggcat ggggcgagcc ggctgtgctg ctgctgctcc tgctgctgag cctggcgctg 1740
 ggcttgtgct tggctgcttt ggggtgttgc gttcaccatc gggacagccc actggttcag 1800
 gcctcggggg gggccctggc ctgctttggc ctgggtgtgc tgggcctggc ctgcctcagc 1860
 gtcctcctgt tccttggcca gcccagccct gcccgatgcc tggcccagca gcccttgtcc 1920
 cacctcccgc tcacgggctg cctgagcaca ctcttctgc aggcggccga gatcttcgtg 1980
 gagtcagaac tgcctctgag ctgggcagac cggctgagtg gctgcctgcg ggggccctgg 2040
 gcctggctgg tgggtgctgt ggccatgctg gtggaggtcg cactgtgcac ctggtacctg 2100
 gtggccttcc cgcggagggt ggtgacggac tggcacatgc tgcccacgga ggcgctggg 2160
 cactgcccga cacgtcctg ggtcagcttc ggcctagcgc acgccacca tgccacgtg 2220
 gcctttctct gcttcttggg cactttcctg gtgcggagcc agccgggctg ctacaaccgt 2280
 gcccgtggcc tcacctttgc catgctggcc tacttcatca cctgggtctc ctttgtgcc 2340
 ctcttggcca atgtgcagg ggtcctcagg cccgccgtgc agatgggcgc cctcctgctc 2400
 tgtgtcctgg gcatcctggc tgccttcac ctgcccaggt gttacctgct catgcggcag 2460
 ccagggtcca acacccccga gttcttcctg ggagggggcc ctggggatgc ccaaggccag 2520
 aatgacggga acacaggaaa tcaggggaaa catgagtga 2559

<210> 10
 <211> 2519
 <212> DNA
 <213> Homo sapiens

<400> 10
 atggggccca gggcaaagac catctgctcc ctgtttctcc tcctatgggt cctggctgag 60
 ccggctgaga actcggactt ctacctgcct ggggattacc tcctgggtgg cctcttctcc 120
 ctccatgcca acatgaaggg cattgttcac cttaacttcc tgcagggtgcc catgtgcaag 180
 gagtatgaag tgaagggtgat aggctacaac ctcatgcagg ccatgcgctt cgcgggtggag 240
 gagatcaaca atgacagcag cctgctgcct ggtgtgctgc tgggctatga gatcgtggat 300
 gtgtgctaca tctccaacaa tgtccagccg gtgctctact tcctggcaca cgaggacaac 360
 ctccttccca tccaagagga ctacagtaac tacatttccc gtgtgggtggc tgtcattggc 420
 cctgacaact ccgagtctgt catgactgtg gccaaacttcc tctccctatt tctccttcca 480
 cagatcacct acagcgcctat cagcgatgag ctgcgagaca aggtgcgctt cccggctttg 540
 ctgcgtacca caccagcgc cgaccaccac gtccgaggcca tgggtgcagct gatgctgcac 600
 ttccgctgga actggatcat tgtgctgggtg agcagcgaca cctatggccg cgacaatggc 660
 agctgcttgg cgagcgcgtg gcccggcgcg acatctgcat cgccttccag gagacgctgc 720
 ccacactgca gcccaaccag aacatgacgt cagaggagcg ccagcgcctg gtgaccattg 780
 tggacaagct gcagcagagc acagcgcgcg tcgtggtcgt gttctcgccc gacctgacct 840
 tgtaccactt cttcaatgag gtgctgcgcc agaacttcac gggcgccgtg tggatcgctt 900
 ccgagtcctg ggccatcgac ccggtcctgc acaacctcac ggagctgggc cacttgggca 960
 ccttctctggg catcaccatc cagagcgtgc ccatcccggt cttcagttag ttccgagagt 1020
 gggggccaca ggctgggccc ccacccctca gcaggaccag ccagagctat acctgcaacc 1080
 aggagtgcga caactgcctg aacgccacct tgccttcaa caccattctc aggtctctctg 1140
 gggagcgtgt cgtctacagc gtgtactctg ccgtctatgc tgtggcccat gccctgcaca 1200
 gcctcctcgg ctgtgacaaa agcacctgca ccaagagggt ggtctacccc tggcagctgc 1260
 ttgaggagat ctggaaggct aacttcactc tcttggaaca ccaaattctc ttcgaccgcg 1320
 aaggggacgt ggctctgcac ttggagattg tccagtggca atgggaccgg agccagaatc 1380
 ccttccagag cgtcgcctcc tactaccccc tgcagcgaca gctgaagaac atccaagaca 1440
 tctcctggga caccgtcaac aacacgatcc ctatgtccat gtgttccaag aggtgccagt 1500
 cagggcaaaa gaagaagcct gtgggcatcc acgtctgctg cttcgagtgc atcgactgcc 1560
 ttcccgccac cttcctcaac cacactgaag atgaatatga atgccaggcc tgcccgaata 1620
 acgagtgggt ctaccagagt gagacctcct gcttcaagcg gcagctgggt ttcttggaat 1680
 ggcattgagg acccaccatc gctgtggccc tgctggccgc cctgggcttc ctcagcacc 1740
 tggccatcct ggtgatattc tggaggcaat tccagacacc catagtctgc tcggctgggg 1800
 gccccatgtg cttcctgatg ctgacactgc tgctgggtggc atacatggtg gtcccgtgt 1860
 acgtggggcc gcccaaggct tccacctgcc tctgccgcca ggccctctt cccctctgct 1920
 tcacaatttg catctcctgt atcgccgtgc gttctttcca gatcgtctgc gccttcaaga 1980
 tggccagccg cttcccacgc gcctacagct actgggtccg ctaccagggg ccctacgtct 2040
 ctatggcatt tatcacggta ctcaaaatgg tcattgtggt aattggcatg ctggccacgg 2100
 gcctcagtc caccaccgt actgaccccg atgaccccaa gatcacaatt gtctcctgta 2160
 accccaacta ccgcaacagc ctgctgttca acaccagcct ggacctgctg ctctcagtgg 2220
 tgggtttcag cttcgcctac atgggcaaag agctgcccac caactacaac gaggccaaagt 2280
 tcatcacct cagcatgacc ttctatttca cctcatccgt ctccctctgc accttcatgt 2340
 ctgcctacag cggggtgctg gtcaccatcg tggacctctt ggtcactgtg ctcaacctcc 2400
 tggccatcag cctgggctac ttcgggccca agtgctacat gatcctcttc taccgggagc 2460
 gcaacacgcc cgcctacttc aacagcatga tccagggtca cccatgagg agggactag 2519

<210> 11
 <211> 2577
 <212> DNA
 <213> Rattus sp.

<400> 11

```

atgccggggt  tggctatctt  gggcctcagt  ctggctgctt  tectggagct  tgggatgggg  60
tcctctttgt  gtctgtcaca  gcaattcaag  gcacaagggg  actatatatt  gggatggacta  120
tttcccctgg  gcacaactga  ggaggccact  ctcaaccaga  gaacacagcc  caacggcatc  180
ctatgtacca  ggttctcgcc  ccttggtttg  ttcctggcca  tggctatgaa  gatggctgta  240
gaggagatca  acaatggatc  tgccttgctc  cctgggctgc  gactgggcta  tgacctgttt  300
gacacatgct  cagagccagt  ggtcaccatg  aagcccagcc  tcatgttcat  ggccaagggtg  360
ggaagtcaaa  gcattgctgc  ctactgcaac  tacacacagt  accaaccctg  tgtgctggct  420
gtcattggtc  cccactcatc  agagcttgcc  ctccattacag  gcaagtctct  cagcttcttc  480
ctcatgccac  aggtcagcta  tagtgccagc  atggatcggc  taagtgaccg  ggaaacattt  540
ccatccttct  tccgcacagt  gccagtgac  cgggtgcagc  tgcaggccgt  tgtgacactg  600
ttgcagaatt  tcagctggaa  ctgggtggct  gccttaggta  gtgatgatga  ctatggccgg  660
gaaggctctga  gcattctttc  tggcttgccc  aactcacgag  gtatctgcat  tgcacacgag  720
ggcctgggtgc  cacaactga  cactagtggc  caacaattgg  gcaagggtgt  ggatgtgcta  780
cgccaagtga  accaaagcaa  agtacagggt  gtgggtgctgt  ttgcatctgc  ccgtgctgtc  840
tactcccttt  ttagctacag  catccttcat  gacctctcac  ccaaggatat  ggtggccagt  900
gagtccctggc  tgacctctga  cctgggtcat  acaacttcca  atattgcccg  tgtgggact  960
gttcttgggt  ttctgcagcg  cggtgcccta  ctgctgaat  tttccatta  tgtggagact  1020
cgccttgccc  tagctgctga  cccaacattc  tgtgcctccc  tgaaagctga  gttggatctg  1080
gaggagcgcg  tgatggggcc  acgctgttca  caatgtgact  acatcatgct  acagaacctg  1140
tcatctgggc  tgatgcagaa  cctatcagct  gggcagttgc  accaccaaat  atttgcaacc  1200
tatgcagctg  tgtacagtgt  ggctcaggcc  cttcacaaca  ccctgcagtg  caatgtctca  1260
cattgccaca  catcagagcc  tgttcaacct  tggcagctcc  tggagaacat  gtacaatatg  1320
agtttccgtg  ctcgagactt  gacactgcag  tttgatgcca  aagggtgtgt  agacatggaa  1380
tatgacctga  agatgtgggt  gtggcagagc  cctacacctg  tactacatac  ttagggcacc  1440
ttcaacggca  ccttccagct  gcagcactcg  aaaatgtatt  ggccaggcaa  ccagggtgcca  1500
gtctcccagt  gctcccggca  gtgcaaagat  ggccagggtg  gcagagtaaa  gggctttcat  1560
tcctgctgct  atgactgtgt  ggactgcaag  gcaggagct  accggaagca  tccagatgac  1620
ttcacctgta  ctccatgtgg  caaggatcag  tgggtcccag  aaaaaagcac  aacctgctta  1680
cctcgaggcc  ccaagtttct  ggcttggggg  gagccagctg  tgctgtcact  tctcctgctg  1740
ctttgcctgg  tgctgggcct  gacactggct  gccctggggc  tctttgtcca  ctactgggac  1800
agccctcttg  ttcaggcctc  aggtgggtca  ctgttctgct  ttggcctgat  ctgcctaggc  1860
ctcttctgce  tcagtgtcct  tctgttccca  ggacgaccac  gctctgccag  ctgccttgcc  1920
caacaaccaa  tggctcacct  cctctcaca  ggctgcctga  gcacactctt  cctgcaagca  1980
gccgagatct  ttgtggagtc  tgagctgcca  ctgagttggg  caaactggct  ctgcagctac  2040
cttcggggcc  cctgggcttg  gctgggtgga  ctgctggcca  ctcttgtgga  ggctgcacta  2100
tgtgcctggg  acttgatggc  tttccctcca  gaggtgggtg  cagattggca  ggtgctgccc  2160
acggaggtag  tggaacactg  ccgcatgcgt  tcctgggtca  gcctgggctt  ggtgcacatc  2220
accaatgcag  tgttagcttt  cctctgcttt  ctgggcactt  tcctggtaca  gagccagcct  2280
ggctgctata  accgtgcccg  tggcctcacc  ttcgccatgc  tagcttattt  catcatctgg  2340
gtctcttttg  tgcccctcct  ggctaattgt  cagggtggcct  accagccagc  tgtgcagatg  2400
ggtgctatct  tattctgtgc  cctgggcac  ctggccacct  tccacctgcc  caaatgctat  2460
gtacttctgt  ggctgccaga  gctcaacacc  caggagttct  tcctgggaag  gagccccaag  2520
gaagcatcag  atgggaatag  tggtagtagt  gaggcacact  ggggacacag  tgaatga  2577

```

<210> 12

<211> 137

<212> PRT

<213> Fugu rubripes

<400> 12

Pro Ser Pro Phe Arg Asp Ile Val Ser Tyr Pro Asp Lys Ile Ile Leu
 1 5 10 15

Gly Cys Phe Met Asn Leu Lys Thr Ser Ser Val Ser Phe Val Leu Leu
 20 25 30

Leu Leu Leu Cys Leu Leu Cys Phe Ile Phe Ser Tyr Met Gly Lys Asp
 35 40 45

Leu Pro Lys Asn Tyr Asn Glu Ala Lys Ala Ile Thr Phe Cys Leu Leu
 50 55 60

Leu Leu Ile Leu Thr Trp Ile Ile Phe Thr Thr Ala Ser Leu Leu Tyr
 65 70 75 80

Gln Gly Lys Tyr Ile His Ser Leu Asn Ala Leu Ala Val Leu Ser Ser
 85 90 95

Ile Tyr Ser Phe Leu Leu Trp Tyr Phe Leu Pro Lys Cys Tyr Ile Ile
 100 105 110

Ile Phe Gln Pro Gln Lys Asn Thr Gln Lys Tyr Phe Gln Gly Leu Ile
 115 120 125

Gln Asp Tyr Thr Lys Thr Ile Ser Gln
 130 135

<210> 13

<211> 242

<212> PRT

<213> Tetraodon cutcutia

<220>

<221> MOD_RES

<222> (120)..(121)

<223> Any amino acid

<400> 13

Phe Ala Val Asn Tyr Asn Thr Pro Val Val Arg Ser Ala Gly Gly Pro
 1 5 10 15

Met Cys Phe Leu Ile Leu Gly Cys Leu Ser Leu Cys Ser Ile Ser Val
 20 25 30

Phe Phe Tyr Phe Glu Arg Pro Thr Glu Ala Phe Cys Ile Leu Arg Phe
 35 40 45

Met Pro Phe Leu Leu Phe Tyr Ala Val Cys Leu Ala Cys Phe Ala Val
 50 55 60

Arg Ser Phe Gln Ile Val Ile Ile Phe Lys Ile Ala Ala Lys Phe Pro
 65 70 75 80

Arg Val His Ser Trp Trp Met Lys Tyr His Gly Gln Trp Leu Val Ile
85 90 95

Ser Met Thr Phe Val Leu Gln Ala Val Val Ile Val Ile Gly Phe Ser
100 105 110

Ser Asn Pro Pro Leu Pro Tyr Xaa Xaa Phe Val Ser Tyr Pro Asp Lys
115 120 125

Ile Ile Leu Gly Cys Asp Val Asn Leu Asn Met Ala Ser Thr Ser Phe
130 135 140

Phe Leu Leu Leu Leu Leu Cys Ile Leu Cys Phe Thr Phe Ser Tyr Met
145 150 155 160

Gly Lys Asp Leu Pro Lys Asn Tyr Asn Glu Ala Lys Ala Ile Thr Phe
165 170 175

Cys Leu Leu Leu Leu Ile Leu Thr Trp Ile Ile Phe Ala Thr Ala Phe
180 185 190

Met Leu Tyr His Gly Lys Tyr Ile His Thr Leu Asn Ala Leu Ala Val
195 200 205

Leu Ser Ser Ala Tyr Cys Phe Leu Leu Trp Tyr Phe Leu Pro Lys Cys
210 215 220

Tyr Ile Ile Ile Phe Gln Pro His Lys Asn Thr Gln Lys Tyr Phe Gln
225 230 235 240

Leu Ser

<210> 14

<211> 165

<212> PRT

<213> Fugu rubripes

<400> 14

Lys Lys Gln Gly Pro Glu Val Asp Ile Phe Ile Val Ser Val Thr Ile
1 5 10 15

Leu Cys Ile Ser Val Leu Gly Val Ala Val Gly Pro Pro Glu Pro Ser
20 25 30

Gln Asp Leu Asp Phe Tyr Met Asp Ser Ile Val Leu Glu Cys Ser Asn
35 40 45

Thr Leu Ser Pro Gly Ser Phe Ile Glu Leu Cys Tyr Val Cys Val Leu
50 55 60

Ser Val Leu Cys Phe Phe Ser Tyr Met Gly Lys Asp Leu Pro Ala
65 70 75 80

Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Met Val Tyr Met
 85 90 95
 Ile Ser Trp Ile Ser Phe Phe Thr Val Tyr Leu Ile Ser Arg Gly Pro
 100 105 110
 Phe Thr Val Ala Ala Tyr Val Cys Ala Thr Leu Val Ser Val Leu Ala
 115 120 125
 Phe Phe Gly Gly Tyr Phe Leu Pro Lys Ile Tyr Ile Ile Val Leu Lys
 130 135 140
 Pro Gln Met Asn Thr Thr Ala His Phe Gln Asn Cys Ile Gln Met Tyr
 145 150 155 160
 Thr Met Ser Lys Gln
 165

<210> 15
 <211> 236
 <212> PRT
 <213> Tetraodon cutcutia

<220>
 <221> MOD_RES
 <222> (8)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (15)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (59)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (62)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (76)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (117)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (128)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (136)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (168)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (173)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (175)..(176)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (203)
 <223> Any amino acid

<220>
 <221> MOD_RES
 <222> (226)
 <223> Any amino acid

<400> 15
 Ala Pro Lys Ser Ser Gln Arg Xaa Leu Arg Arg Thr Arg Leu Xaa Leu
 1 5 10 15
 Glu Trp Asp His Pro Met Ser Val Ala Leu Leu Phe Phe Leu Val Cys
 20 25 30
 Cys Leu Leu Met Thr Ser Ser Ser Ala Val Ile Leu Leu Leu Asn Ile
 35 40 45
 Asn Thr Pro Val Ala Lys Ser Ala Gly Gly Xaa Thr Cys Xaa Leu Lys
 50 55 60
 Leu Ala Ala Leu Thr Ala Ala Ala Met Ser Ser Xaa Cys His Phe Gly
 65 70 75 80
 Gln Pro Ser Pro Leu Ala Ser Lys Leu Lys Gln Pro Gln Phe Thr Phe
 85 90 95

Ser Phe Thr Val Cys Leu Ala Cys Asn Arg Cys Ala Leu Ala Thr Gly
 100 105 110

His Leu His Phe Xaa Ile Arg Val Ala Leu Pro Pro Ala Tyr Asn Xaa
 115 120 125

Trp Ala Lys Asn His Gly Pro Xaa Ala Thr Ile Phe Ile Ala Ser Ala
 130 135 140

Ala Ile Leu Cys Val Leu Cys Leu Arg Val Ala Val Gly Pro Pro Gln
 145 150 155 160

Pro Ser Gln Asx Leu Asx Phe Xaa Thr Asn Ser Ile Xaa Leu Xaa Xaa
 165 170 175

Ser Asn Thr Leu Ser Pro Gly Ser Phe Val Glu Leu Cys Asn Val Ser
 180 185 190

Leu Leu Ser Ala Val Cys Phe Val Phe Ser Xaa Met Gly Lys Asx Leu
 195 200 205

Pro Ala Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Met Val
 210 215 220

Asn Xaa Ile Ser Trp Ile Ser Phe Phe Thr Val Tyr
 225 230 235

<210> 16
 <211> 840
 <212> PRT
 <213> Rattus sp.

<400> 16
 Met Leu Phe Trp Ala Ala His Leu Leu Leu Ser Leu Gln Leu Val Tyr
 1 5 10 15

Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly Phe Ser
 20 25 30

Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His Gly Asp
 35 40 45

Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp Arg Pro
 50 55 60

Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met Arg Phe
 65 70 75 80

Thr Val Glu Glu Ile Asn Asn Ser Ser Ala Leu Leu Pro Asn Ile Thr
 85 90 95

Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ala Asn Val Tyr
 100 105 110
 Ala Thr Leu Arg Val Leu Ala Leu Gln Gly Pro Arg His Ile Glu Ile
 115 120 125
 Gln Lys Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Phe Ile Gly
 130 135 140
 Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu Gly Pro
 145 150 155 160
 Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Val Leu Ser
 165 170 175
 Ala Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Arg
 180 185 190
 His Gln Val Glu Val Met Val Gln Leu Leu Gln Ser Phe Gly Trp Val
 195 200 205
 Trp Ile Ser Leu Ile Gly Ser Tyr Gly Asp Tyr Gly Gln Leu Gly Val
 210 215 220
 Gln Ala Leu Glu Glu Leu Ala Val Pro Arg Gly Ile Cys Val Ala Phe
 225 230 235 240
 Lys Asp Ile Val Pro Phe Ser Ala Arg Val Gly Asp Pro Arg Met Gln
 245 250 255
 Ser Met Met Gln His Leu Ala Gln Ala Arg Thr Thr Val Val Val Val
 260 265 270
 Phe Ser Asn Arg His Leu Ala Arg Val Phe Phe Arg Ser Val Val Leu
 275 280 285
 Ala Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Asp Trp Ala Ile
 290 295 300
 Ser Thr Tyr Ile Thr Ser Val Thr Gly Ile Gln Gly Ile Gly Thr Val
 305 310 315 320
 Leu Gly Val Ala Val Gln Gln Arg Gln Val Pro Gly Leu Lys Glu Phe
 325 330 335
 Glu Glu Ser Tyr Val Arg Ala Val Thr Ala Ala Pro Ser Ala Cys Pro
 340 345 350
 Glu Gly Ser Trp Cys Ser Thr Asn Gln Leu Cys Arg Glu Cys His Thr
 355 360 365
 Phe Thr Thr Arg Asn Met Pro Thr Leu Gly Ala Phe Ser Met Ser Ala
 370 375 380

Ala Tyr Arg Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly Leu His
 385 390 395 400
 Gln Leu Leu Gly Cys Thr Ser Glu Ile Cys Ser Arg Gly Pro Val Tyr
 405 410 415
 Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu Leu His
 420 425 430
 Glu Asn Thr Val Ala Phe Asp Asp Asn Gly Asp Thr Leu Gly Tyr Tyr
 435 440 445
 Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe Glu Ile
 450 455 460
 Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn Lys Thr
 465 470 475 480
 Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser Val Cys
 485 490 495
 Thr Thr Asp Cys Leu Ala Gly His His Arg Val Val Val Gly Ser His
 500 505 510
 His Cys Cys Phe Glu Cys Val Pro Cys Glu Ala Gly Thr Phe Leu Asn
 515 520 525
 Met Ser Glu Leu His Ile Cys Gln Pro Cys Gly Thr Glu Glu Trp Ala
 530 535 540
 Pro Lys Glu Ser Thr Thr Cys Phe Pro Arg Thr Val Glu Phe Leu Ala
 545 550 555 560
 Trp His Glu Pro Ile Ser Leu Val Leu Ile Ala Ala Asn Thr Leu Leu
 565 570 575
 Leu Leu Leu Leu Val Gly Thr Ala Gly Leu Phe Ala Trp His Phe His
 580 585 590
 Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met Leu
 595 600 605
 Gly Ser Leu Val Ala Gly Ser Cys Ser Phe Tyr Ser Phe Phe Gly Glu
 610 615 620
 Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser Leu Gly
 625 630 635 640
 Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln Leu Val
 645 650 655
 Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr Arg Thr Trp
 660 665 670

Ala Gln Asn His Gly Ala Gly Leu Phe Val Ile Val Ser Ser Thr Val
675 680 685

His Leu Leu Ile Cys Leu Thr Trp Leu Val Met Trp Thr Pro Arg Pro
690 695 700

Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu Cys Thr
705 710 715 720

Glu Val Asn Ser Val Gly Phe Leu Leu Ala Phe Thr His Asn Ile Leu
725 730 735

Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu Leu Pro
740 745 750

Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Leu Asn
755 760 765

Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ala Ser Ile Tyr Gln Gly
770 775 780

Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Thr Thr Leu Ser
785 790 795 800

Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys
805 810 815

Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile Gln Asp
820 825 830

Tyr Thr Arg Arg Cys Gly Thr Thr
835 840

<210> 17
<211> 843
<212> PRT
<213> Rattus sp.

<400> 17
Met Gly Pro Gln Ala Arg Thr Leu Cys Leu Leu Ser Leu Leu Leu His
1 5 10 15

Val Leu Pro Lys Pro Gly Lys Leu Val Glu Asn Ser Asp Phe His Leu
20 25 30

Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val
35 40 45

Lys Ser Ile Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu
50 55 60

Phe Thr Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe
65 70 75 80

Ala	Val	Glu	Glu	Ile	Asn	Asn	Cys	Ser	Ser	Leu	Leu	Pro	Gly	Val	Leu	
				85					90						95	
Leu	Gly	Tyr	Glu	Met	Val	Asp	Val	Cys	Tyr	Leu	Ser	Asn	Asn	Ile	His	
			100					105					110			
Pro	Gly	Leu	Tyr	Phe	Leu	Ala	Gln	Asp	Asp	Asp	Leu	Leu	Pro	Ile	Leu	
		115					120					125				
Lys	Asp	Tyr	Ser	Gln	Tyr	Met	Pro	His	Val	Val	Ala	Val	Ile	Gly	Pro	
	130					135					140					
Asp	Asn	Ser	Glu	Ser	Ala	Ile	Thr	Val	Ser	Asn	Ile	Leu	Ser	His	Phe	
145					150					155					160	
Leu	Ile	Pro	Gln	Ile	Thr	Tyr	Ser	Ala	Ile	Ser	Asp	Lys	Leu	Arg	Asp	
				165					170					175		
Lys	Arg	His	Phe	Pro	Ser	Met	Leu	Arg	Thr	Val	Pro	Ser	Ala	Thr	His	
			180					185					190			
His	Ile	Glu	Ala	Met	Val	Gln	Leu	Met	Val	His	Phe	Gln	Trp	Asn	Trp	
		195					200					205				
Ile	Val	Val	Leu	Val	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Asn	Ser	His	
	210					215					220					
Leu	Leu	Ser	Gln	Arg	Leu	Thr	Lys	Thr	Ser	Asp	Ile	Cys	Ile	Ala	Phe	
225					230					235					240	
Gln	Glu	Val	Leu	Pro	Ile	Pro	Glu	Ser	Ser	Gln	Val	Met	Arg	Ser	Glu	
				245					250					255		
Glu	Gln	Arg	Gln	Leu	Asp	Asn	Ile	Leu	Asp	Lys	Leu	Arg	Arg	Thr	Ser	
			260					265					270			
Ala	Arg	Val	Val	Val	Val	Phe	Ser	Pro	Glu	Leu	Ser	Leu	Tyr	Ser	Phe	
		275					280					285				
Phe	His	Glu	Val	Leu	Arg	Trp	Asn	Phe	Thr	Gly	Phe	Val	Trp	Ile	Ala	
	290					295					300					
Ser	Glu	Ser	Trp	Ala	Ile	Asp	Pro	Val	Leu	His	Asn	Leu	Thr	Glu	Leu	
305					310					315					320	
Arg	His	Thr	Gly	Thr	Phe	Leu	Gly	Val	Thr	Ile	Gln	Arg	Val	Ser	Ile	
				325					330					335		
Pro	Gly	Phe	Ser	Gln	Phe	Arg	Val	Arg	Arg	Asp	Lys	Pro	Gly	Tyr	Pro	
			340					345					350			
Val	Pro	Asn	Thr	Thr	Asn	Leu	Arg	Thr	Thr	Cys	Asn	Gln	Asp	Cys	Asp	
		355					360					365				

Ala Cys Leu Asn Thr Thr Lys Ser Phe Asn Asn Ile Leu Ile Leu Ser
 370 375 380
 Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala
 385 390 395 400
 His Ala Leu His Arg Leu Leu Gly Cys Asn Arg Val Arg Cys Thr Lys
 405 410 415
 Gln Lys Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn
 420 425 430
 Phe Thr Leu Leu Gly Asn Arg Leu Phe Phe Asp Gln Gln Gly Asp Met
 435 440 445
 Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Asp Leu Ser Gln Asn
 450 455 460
 Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Ser Lys Arg Leu Thr
 465 470 475 480
 Tyr Ile Asn Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Val
 485 490 495
 Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Ser Val
 500 505 510
 Gly Leu His Pro Cys Cys Phe Glu Cys Leu Asp Cys Met Pro Gly Thr
 515 520 525
 Tyr Leu Asn Arg Ser Ala Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly
 530 535 540
 Ser Met Trp Ser Tyr Lys Asn Asp Ile Thr Cys Phe Gln Arg Arg Pro
 545 550 555 560
 Thr Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Ala Ile Leu
 565 570 575
 Ala Ala Leu Gly Phe Phe Ser Thr Leu Ala Ile Leu Phe Ile Phe Trp
 580 585 590
 Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys
 595 600 605
 Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val
 610 615 620
 Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe
 625 630 635 640
 Phe Thr Val Cys Phe Ser Ile Cys Leu Ser Cys Ile Thr Val Arg Ser
 645 650 655

Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala
660 665 670

Tyr Ser Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe
675 680 685

Ile Thr Ala Ile Lys Val Ala Leu Val Val Gly Asn Met Leu Ala Thr
690 695 700

Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Met
705 710 715 720

Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr
725 730 735

Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Met
740 745 750

Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu
755 760 765

Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met
770 775 780

Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr
785 790 795 800

Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys
805 810 815

Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn
820 825 830

Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser
835 840

<210> 18

<211> 845

<212> PRT

<213> Rattus sp.

<400> 18

Met Val Arg Leu Leu Leu Ile Phe Phe Pro Met Ile Phe Leu Glu Met
1 5 10 15

Ser Ile Leu Pro Arg Met Pro Asp Arg Lys Val Leu Leu Ala Gly Ala
20 25 30

Ser Ser Gln Arg Ser Val Ala Arg Met Asp Gly Asp Val Ile Ile Gly
35 40 45

Ala Leu Phe Ser Val His His Gln Pro Pro Ala Glu Lys Val Pro Glu
 50 55 60

Arg Lys Cys Gly Glu Ile Arg Glu Gln Tyr Gly Ile Gln Arg Val Glu
 65 70 75 80

Ala Met Phe His Thr Leu Asp Lys Ile Asn Ala Asp Pro Val Leu Leu
 85 90 95

Pro Asn Ile Thr Leu Gly Ser Glu Ile Arg Asp Ser Cys Trp His Ser
 100 105 110

Ser Val Ala Leu Glu Gln Ser Ile Glu Phe Ile Arg Asp Ser Leu Ile
 115 120 125

Ser Ile Arg Asp Glu Lys Asp Gly Leu Asn Arg Cys Leu Pro Asp Gly
 130 135 140

Gln Thr Leu Pro Pro Gly Arg Thr Lys Lys Pro Ile Ala Gly Val Ile
 145 150 155 160

Gly Pro Gly Ser Ser Ser Val Ala Ile Gln Val Gln Asn Leu Leu Gln
 165 170 175

Leu Phe Asp Ile Pro Gln Ile Ala Tyr Ser Ala Thr Ser Ile Asp Leu
 180 185 190

Ser Asp Lys Thr Leu Tyr Lys Tyr Phe Leu Arg Val Val Pro Ser Asp
 195 200 205

Thr Leu Gln Ala Arg Ala Met Leu Asp Ile Val Lys Arg Tyr Asn Trp
 210 215 220

Thr Tyr Val Ser Ala Val His Thr Glu Gly Asn Tyr Gly Glu Ser Gly
 225 230 235 240

Met Asp Ala Phe Lys Glu Leu Ala Ala Gln Glu Gly Leu Cys Ile Ala
 245 250 255

His Ser Asp Lys Ile Tyr Ser Asn Ala Gly Glu Lys Ser Phe Asp Arg
 260 265 270

Leu Leu Arg Lys Leu Arg Glu Arg Leu Pro Lys Ala Arg Val Val Val
 275 280 285

Cys Phe Cys Glu Gly Met Thr Val Arg Gly Leu Leu Ser Ala Met Arg
 290 295 300

Arg Leu Gly Val Val Gly Glu Phe Ser Leu Ile Gly Ser Asp Gly Trp
 305 310 315 320

Ala Asp Arg Asp Glu Val Ile Glu Gly Tyr Glu Val Glu Ala Asn Gly
 325 330 335

Gly Ile Thr Ile Lys Leu Gln Ser Pro Glu Val Arg Ser Phe Asp Asp
 340 345 350
 Tyr Phe Leu Lys Leu Arg Leu Asp Thr Asn Thr Arg Asn Pro Trp Phe
 355 360 365
 Pro Glu Phe Trp Gln His Arg Phe Gln Cys Arg Leu Pro Gly His Leu
 370 375 380
 Leu Glu Asn Pro Asn Phe Lys Lys Val Cys Thr Gly Asn Glu Ser Leu
 385 390 395 400
 Glu Glu Asn Tyr Val Gln Asp Ser Lys Met Gly Phe Val Ile Asn Ala
 405 410 415
 Ile Tyr Ala Met Ala His Gly Leu Gln Asn Met His His Ala Leu Cys
 420 425 430
 Pro Gly His Val Gly Leu Cys Asp Ala Met Lys Pro Ile Asp Gly Arg
 435 440 445
 Lys Leu Leu Asp Phe Leu Ile Lys Ser Ser Phe Val Gly Val Ser Gly
 450 455 460
 Glu Glu Val Trp Phe Asp Glu Lys Gly Asp Ala Pro Gly Arg Tyr Asp
 465 470 475 480
 Ile Met Asn Leu Gln Tyr Thr Glu Ala Asn Arg Tyr Asp Tyr Val His
 485 490 495
 Val Gly Thr Trp His Glu Gly Val Leu Asn Ile Asp Asp Tyr Lys Ile
 500 505 510
 Gln Met Asn Lys Ser Gly Met Val Arg Ser Val Cys Ser Glu Pro Cys
 515 520 525
 Leu Lys Gly Gln Ile Lys Val Ile Arg Lys Gly Glu Val Ser Cys Cys
 530 535 540
 Trp Ile Cys Thr Ala Cys Lys Glu Asn Glu Phe Val Gln Asp Glu Phe
 545 550 555 560
 Thr Cys Arg Ala Cys Asp Leu Gly Trp Trp Pro Asn Ala Glu Leu Thr
 565 570 575
 Gly Cys Glu Pro Ile Pro Val Arg Tyr Leu Glu Trp Ser Asp Ile Glu
 580 585 590
 Ser Ile Ile Ala Ile Ala Phe Ser Cys Leu Gly Ile Leu Val Thr Leu
 595 600 605
 Phe Val Thr Leu Ile Phe Val Leu Tyr Arg Asp Thr Pro Val Val Lys
 610 615 620

Ser Ser Ser Arg Glu Leu Cys Tyr Ile Ile Leu Ala Gly Ile Phe Leu
625 630 635 640

Gly Tyr Val Cys Pro Phe Thr Leu Ile Ala Lys Pro Thr Thr Thr Ser
645 650 655

Cys Tyr Leu Gln Arg Leu Leu Val Gly Leu Ser Ser Ala Met Cys Tyr
660 665 670

Ser Ala Leu Val Thr Lys Thr Asn Arg Ile Ala Arg Ile Leu Ala Gly
675 680 685

Ser Lys Lys Lys Ile Cys Thr Arg Lys Pro Arg Phe Met Ser Ala Trp
690 695 700

Ala Gln Val Ile Ile Ala Ser Ile Leu Ile Ser Val Gln Leu Thr Leu
705 710 715 720

Val Val Thr Leu Ile Ile Met Glu Pro Pro Met Pro Ile Leu Ser Tyr
725 730 735

Pro Ser Ile Lys Glu Val Tyr Leu Ile Cys Asn Thr Ser Asn Leu Gly
740 745 750

Val Val Ala Pro Val Gly Tyr Asn Gly Leu Leu Ile Met Ser Cys Thr
755 760 765

Tyr Tyr Ala Phe Lys Thr Arg Asn Val Pro Ala Asn Phe Asn Glu Ala
770 775 780

Lys Tyr Ile Ala Phe Thr Met Tyr Thr Thr Cys Ile Ile Trp Leu Ala
785 790 795 800

Phe Val Pro Ile Tyr Phe Gly Ser Asn Tyr Lys Ile Ile Thr Thr Cys
805 810 815

Phe Ala Val Ser Leu Ser Val Thr Val Ala Leu Gly Cys Met Phe Thr
820 825 830

Pro Lys Met Tyr Ile Ile Ile Ala Lys Pro Glu Arg Asn
835 840 845

<210> 19

<211> 867

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala Leu Thr Trp His
1 5 10 15

Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
20 25 30

Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
 35 40 45
 Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
 50 55 60
 Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
 65 70 75 80
 Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
 85 90 95
 Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
 100 105 110
 Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
 115 120 125
 Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
 130 135 140
 Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
 145 150 155 160
 Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
 165 170 175
 Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His
 180 185 190
 Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
 195 200 205
 Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
 210 215 220
 Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser
 225 230 235 240
 Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
 245 250 255
 Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
 260 265 270
 Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
 275 280 285
 Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
 290 295 300
 Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
 305 310 315 320

Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
 325 330 335
 Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
 340 345 350
 Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
 355 360 365
 Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
 370 375 380
 Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
 385 390 395 400
 Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
 405 410 415
 Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
 420 425 430
 Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
 435 440 445
 Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
 450 455 460
 Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
 465 470 475 480
 Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
 485 490 495
 Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
 500 505 510
 Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
 515 520 525
 Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
 530 535 540
 Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr
 545 550 555 560
 Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu
 565 570 575
 Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn
 580 585 590
 Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp
 595 600 605

Thr Glu Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly Ile
 610 615 620
 Phe Leu Thr Ala Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr
 625 630 635 640
 Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe
 645 650 655
 Ser Leu Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro
 660 665 670
 Gln Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe
 675 680 685
 Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu
 690 695 700
 Val Phe Glu Ala Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly
 705 710 715 720
 Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile
 725 730 735
 Val Ile Cys Val Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg
 740 745 750
 Asn Gln Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly
 755 760 765
 Ser Leu Met Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala
 770 775 780
 Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn
 785 790 795 800
 Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile
 805 810 815
 Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe
 820 825 830
 Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu
 835 840 845
 Leu Ala Cys Ile Phe Phe Asn Lys Ile Tyr Ile Ile Leu Phe Lys Pro
 850 855 860
 Ser Arg Asn
 865